

> d his

(FILE 'HOME' ENTERED AT 09:32:43 ON 31 MAY 2006)

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:32:46 ON 31 MAY 2006

L1 10280 S RHODOCOCCUS
L2 234 S L1 (10N) DEHYDROGENASE
L3 156 DUP REM L2 (78 DUPLICATES REMOVED)
L4 67 S L3 AND ALCOHOL
L5 40 S L4 AND PY<2003
L6 2 S L5 AND RUBER

FILE 'STNGUIDE' ENTERED AT 09:35:04 ON 31 MAY 2006

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:43:15 ON 31 MAY 2006

L7 12 S L3 AND RUBER
L8 12 DUP REM L7 (0 DUPLICATES REMOVED)
L9 113 S L3 AND PY<2003
L10 4 S L8 AND PY<2003

FILE 'STNGUIDE' ENTERED AT 09:48:34 ON 31 MAY 2006

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:49:25 ON 31 MAY 2006

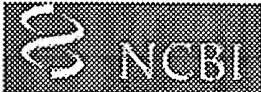

FILE 'STNGUIDE' ENTERED AT 09:50:31 ON 31 MAY 2006

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:52:39 ON 31 MAY 2006

L11 10 S L5 AND (STERO? OR KDA OR DA OR ZN)
L12 17 S L5 AND (STER? OR OPTI? OR KDA OR DA OR ZN)

FILE 'STNGUIDE' ENTERED AT 09:55:13 ON 31 MAY 2006

	Type	L #	Hits	Search Text
1	BRS	L1	2856	rhodococcus
2	BRS	L2	235	l1 and (alcohol near2 dehydrogenase)
3	BRS	L3	29	l2 and ruber
4	BRS	L4	26	l2 and (rhodococcus near2 ruber)
5	BRS	L5	2	(alcohol near2 dehydrogenase) near10 (rhodococcus near2 ruber)
6	BRS	L6	16	(alcohol near2 dehydrogenase) near10 (rhodococcus)

My NCBI
[\[Sign In\]](#) [\[Reg\]](#)

[All Databases](#) [PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [PMC](#) [Taxonomy](#) [Bo](#)

Search Protein for txid1830[Organism:noexp] AND dehydrogenase
Preview
Go
C

[Limits](#) [Preview/Index](#) **[History](#)** [Clipboard](#) [Details](#)

About Entrez

Entrez Protein
[Help](#) | [FAQ](#)

Entrez Tools

Check sequence
 revision history

LinkOut

My NCBI (Cubby)

Related resources
 BLAST

Reference sequence
 project

Search for Genes

Clusters of orthologous
 groups

Protein reviews on the
 web

Search for full length
 cDNAs

- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

Search	Most Recent Queries	Time	Result
#17	Search txid1830[Organism:noexp] AND dehydrogenase	12:33:03	14
#16	Search txid1830[Organism:noexp]	12:32:59	58
#13	Protein Links for PubMed (Select 10531651)	12:31:11	2

Clear History

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

May 22 2006 06:31:57

RESULT 1

US-10-004-115B-34

; Sequence 34, Application US/10004115B
 ; Patent No. 6884607
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAKO, HIROYUKI
 ; APPLICANT: MATSUMURA, KENJI
 ; APPLICANT: SHIMIZU, MASATOSHI
 ; APPLICANT: ITO, NOBUYA
 ; APPLICANT: WAKITA, RYUHEI
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
 ; TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE
 ; FILE REFERENCE: 7372-72249
 ; CURRENT APPLICATION NUMBER: US/10/004,115B
 ; CURRENT FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: JP 2000-372704
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: JP 2001-006144
 ; PRIOR FILING DATE: 2001-01-15
 ; PRIOR APPLICATION NUMBER: JP 2001-026594
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: JP 2001-175175
 ; PRIOR FILING DATE: 2001-06-11
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 34
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium sp.
 US-10-004-115B-34

Query Match 64.9%; Score 1152.5; DB 2; Length 348;
 Best Local Similarity 63.6%; Pred. No. 1.8e-101;
 Matches 220; Conservative 40; Mismatches 85; Indels 1; Gaps 1;

Qy	1	MKAVQYTEIGSEPVVVDIPTPTPGPGEILLKVTAAGLCHSDIFVMDMPAAQYAYGLPLTL	60
		: : : :	
Db	1	MKAIQYTRIGAEPTELTEIPKPEPGPGEVLLVTAAGVCHSDDFIMSLPEEQYTYGLPLTL	60
Qy	61	GHEGVGTVAELGEGVTGFGVGDAVAVYGPWGCACHACARGRENYCTRAADLGITPPGLG	120
		: : :	
Db	61	GHEGAGKVAAVGEGVEGLDIGTNVVVYGPWGCNCWHCSQGLENYCSRAQELGINPPGLG	120
Qy	121	SPGSMAEYMIVDSARHLVPIGDLDPVAAAPLTDAGLTPYHAISRVLPLLPGPGSTAVVIGV	180
		: : :	
Db	121	APGALAEFMIVDSPRHLVPIGDLDPVKTVPLTDAGLTPYHAIKRSLPKLRGGSYAVVIGT	180
Qy	181	GGLGHVGIQILRAVSAARVIAVDLDDRLALAREVGADAAVKSGAGAADAIRELTGGQGA	240
		: : : : :	
Db	181	GGLGHVAIQLRLHLSAATVIALDVSADKLELATKVGAEVVLSDKDAENVRKITGSQGA	240
Qy	241	TAVFDFVGAQSTIDTAQQVAVDGHISVVGIIHAG-AHAKVGFFMIPFGASVVTPTYWGTRS	299
Db	241	ALVLDVFGVYQPTIDTAMAVAGVGSVDVTIVGIGDQGAHAKVGFFQSPYEASVTVPYWGARN	300
Qy	300	ELMEVVALARAGRLDIHTETFTLDEGPAAYRRLREGSIRGRGVVVP	345
		: :	
Db	301	ELIELIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTSLGRAVVVP	346

Db

Qy

Db

Qy

Db

Qy

Db

RESULT 1

US-09-252-991A-26632

; Sequence 26632, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 26632

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26632

Query Match 90.7%; Score 39; DB 2; Length 233;

Best Local Similarity 80.0%; Pred. No. 17;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGAGAADAXR 10

:|||||||

Db 18 AGAGAADARR 27

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	35	81.4	123	2	H81235	50S ribosomal prot
2	34	79.1	255	2	JC7264	CCAAT-enhancer bin
3	34	79.1	263	2	B75361	WD-repeat family p
4	34	79.1	525	2	AF3274	hypothetical prote
5	34	79.1	547	1	S51475	cytochrome P450 cy
6	34	79.1	602	2	H87503	phosphogluconate d
7	34	79.1	741	2	D75500	ATP-dependent Clp
8	34	79.1	1335	2	H75511	DNA polymerase III
9	33	76.7	299	2	F75295	hypothetical prote
10	33	76.7	370	2	A60089	transforming prote
11	33	76.7	397	2	T35609	whiE protein I - S
12	33	76.7	428	2	S17817	bacteriochlorophyl
13	33	76.7	461	2	T51030	probable acetylorn
14	33	76.7	463	2	T34841	probable bifunctio
15	33	76.7	588	2	AC0611	transport ATP-bind
16	33	76.7	588	2	B85614	hypothetical prote
17	33	76.7	588	2	D90750	hypothetical prote
18	33	76.7	588	2	F64827	ABC-type

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	97.7	346	2	Q8KLT9_9NOCA	Q8klt9 rhodococcus
2	39	90.7	478	2	Q82F52_STRAW	Q82f52 streptomyce
3	38	88.4	557	2	Q2T4A0_BURTH	Q2t4a0 burkholderi
4	38	88.4	581	2	Q5KGT5_CRYNE	Q5kgt5 cryptococcu
5	38	88.4	613	2	Q55SE1_CRYNE	Q55se1 cryptococcu
6	38	88.4	964	2	Q4KXA8_LEIME	Q4kxa8 leishmania
7	37	86.0	737	2	Q8LTQ2_9CAUD	Q8ltq2 lactococcus
8	36	83.7	241	2	Q651U8_ORYSA	Q65lu8 oryza sativ
9	36	83.7	248	2	Q84R34_ORYSA	Q84r34 oryza sativ
10	36	83.7	379	2	Q3GCC8_9FIRM	Q3gcc8 syntrophomo
11	35	81.4	73	2	Q7R475_GIALA	Q7r475 giardia lam
12	35	81.4	81	2	Q341E1_RHOPA	Q341e1 rhodopseudo
13	35	81.4	122	1	RL7_NEIMA	P0a0x0 neisseria m
14	35	81.4	122	1	RL7_NEIMB	P0a0x1 neisseria m
15	35	81.4	123	2	Q5F5R4_NEIG1	Q5f5r4 neisseria g
16	35	81.4	132	2	Q4DER8_TRYCR	Q4der8 trypanosoma
17	35	81.4	135	2	Q4D9Q6_TRYCR	Q4d9q6 trypanosoma
18	35	81.4	296	2	P72540_STRPR	

RESULT 1

Q8KLT9_9NOCA

ID Q8KLT9_9NOCA PRELIMINARY; PRT; 346 AA.

AC Q8KLT9;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE Secondary alcohol dehydrogenase (EC 1.1.1.1).

GN Name=sadh;

OS Rhodococcus ruber.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI_TaxID=1830;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=219;

RA Tamak C., Plattner H., Hummel W., Diekmann H., Meens J.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- COFACTOR: Zinc (By similarity).

 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

DR EMBL; AJ491307; CAD36475.1; -; Genomic_DNA.

DR HSSP; Q59096; 1F8F.

DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR013154; ADH_N.

DR InterPro; IPR002085; ADH_Sf_Zn.

DR InterPro; IPR002328; ADH_Zn.

DR InterPro; IPR013149; ADH_Zn_bd.

DR InterPro; IPR002110; ANK.

DR PANTHER; PTHR11695; Adh_zn_family; 1.

DR PRINTS; PR01415; ANKYRIN.

DR PROSITE; PS00059; ADH_ZINC; 1.

KW Metal-binding; NAD; Oxidoreductase; Zinc.

SQ SEQUENCE 346 AA; 35449 MW; F885D8B0F7E6C1CC CRC64;

Query Match 97.7%; Score 42; DB 2; Length 346;

Best Local Similarity 90.0%; Pred. No. 27;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGAGAADAXR 10

|||||||

Db 223 SGAGAADAIR 232

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1775	100.0	345	9	ADY85204	Ady85204 Rhodococc
2	1188.5	67.0	346	9	ADZ03703	Adz03703 Streptomy
3	1152.5	64.9	348	8	ADL18256	Adl18256 Corynebac
4	1152.5	64.9	348	9	ADV69575	Adv69575 Corynebac
5	1151.5	64.9	348	7	ADF53768	Adf53768 Alcohol d
6	1150.5	64.8	348	9	AED84856	Aed84856 Alcohol d
7	1145.5	64.5	348	9	AED84855	Aed84855 Alcohol d
8	1100.5	62.0	344	8	ADN25583	Adn25583 Bacterial
9	1061.5	59.8	384	8	ADK70245	Adk70245 Corynebac
10	1061.5	59.8	385	5	AAO21525	Aao21525 385-mer C
11	1061.5	59.8	385	5	ABB77974	Abb77974 Amino aci
12	1061.5	59.8	385	7	ADE39627	Ade39627 Corynebac
13	1061.5	59.8	385	8	ADF88657	Adf88657 3-quinucl
14	1061.5	59.8	385	8	ADK82546	Adk82546 Isomerase
15	1061.5	59.8	385	8	ADM46684	Adm46684 385 amino
16	1061.5	59.8	385	8	ADM46565	Adm46565 Corynebac
17	916.5	51.6	327	8	ADN25512	Adn25512 Bacterial
18	577	32.5	162	9	AED84825	Aed84825 Alcohol d
19	559	31.5	161	9	AED84826	Aed84826 Alcohol d
20	556	31.3	162	9	AED84823	Aed84823 Alcohol d
21	533	30.0	341	9	ADZ47402	Adz47402 341 amino
22	480.5	27.1	359	8	ADS44521	Ads44521 Bacterial
23	476	26.8	128	9	AED84824	

Database : Issued_Patents_AA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1152.5	64.9	348	2	US-10-004-115B-34	Sequence 34, Appl
2	1061.5	59.8	385	2	US-09-984-334-1	Sequence 1, Appli
3	481.5	27.1	352	2	US-09-504-358-18	Sequence 18, Appl
4	481.5	27.1	352	2	US-09-954-314-18	Sequence 18, Appl
5	481.5	27.1	352	2	US-10-230-562-18	Sequence 18, Appl
6	465.5	26.2	352	2	US-09-648-004-24	Sequence 24, Appl
7	465.5	26.2	352	2	US-10-272-419-24	Sequence 24, Appl
8	463.5	26.1	381	2	US-09-248-796A-20906	Sequence 20906, A
9	422.5	23.8	336	1	US-08-713-254-2	Sequence 2, Appli
10	422.5	23.8	336	2	US-08-855-767-2	Sequence 2, Appli
11	414.5	23.4	346	2	US-09-489-039A-9885	Sequence 9885, Ap
12	403	22.7	344	2	US-09-134-001C-5343	Sequence 5343, Ap
13	394.5	22.2	465	2	US-09-252-991A-18919	Sequence 18919, A
14	374.5	21.1	375	2	US-09-134-000C-5937	Sequence

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1775	100.0	345	4	US-10-666-205-48	Sequence 48, Appl
2	1713	96.5	346	6	US-11-087-099-9022	Sequence 9022, Ap
3	1152.5	64.9	348	5	US-10-617-034A-1	Sequence 1, Appli
4	1151.5	64.9	348	6	US-11-188-298-13982	Sequence 13982, A
5	1100.5	62.0	344	4	US-10-369-493-8236	Sequence 8236, Ap
6	1061.5	59.8	385	3	US-09-984-334-1	Sequence 1, Appli
7	1061.5	59.8	385	4	US-10-004-115A-34	Sequence 34, Appl
8	1061.5	59.8	385	4	US-10-327-108-1	Sequence 1, Appli
9	1061.5	59.8	385	5	US-10-920-239-34	Sequence 34, Appl
10	1061.5	59.8	385	6	US-11-087-099-1453	Sequence 1453, Ap
11	1061.5	59.8	385	6	US-11-188-298-1461	Sequence 1461, Ap
12	933.5	52.6	360	6	US-11-188-298-5305	Sequence 5305, Ap
13	916.5	51.6	327	4	US-10-369-493-8165	Sequence 8165, Ap
14	606	34.1	341	4	US-10-156-761-8932	Sequence

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	526	29.6	344	2	D90325	alcohol dehydrogen
2	480.5	27.1	359	2	C72533	probable alcohol d
3	472	26.6	347	1	S51120	alcohol dehydrogen
4	465	26.2	347	1	A44245	alcohol dehydrogen
5	455.5	25.7	349	2	B90285	alcohol dehydrogen
6	451.5	25.4	340	2	T37030	alcohol dehydrogen
7	445.5	25.1	236	2	T36399	probable alcohol d
8	442	24.9	346	2	H81915	probable alcohol d
9	442	24.9	348	2	H81186	probable alcohol d
10	419.5	23.6	336	2	AH0672	alcohol dehydrogen
11	419	23.6	365	2	T36806	probable alcohol d
12	417.5	23.5	342	2	H97434	alcohol dehydrogen
13	417.5	23.5	342	2	AD2653	alcohol dehydrogen
14	415	23.4	346	1	A64901	alcohol dehydrogen
15	415	23.4	346	2	G85728	alcohol dehydrogen

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1713	96.5	346	2	Q8KLT9_9NOCA	Q8klt9 rhodococcus
2	1188.5	67.0	346	2	Q9S5E6_STRCO	Q9s5e6 streptomyce
3	1168.5	65.8	348	2	Q415U1_KINRA	Q415u1 kineococcus
4	1152.5	64.9	348	2	Q65YQ4_9NOCA	Q65yq4 rhodococcus
5	1151.5	64.9	348	2	Q6YBW1_RHOER	Q6ybw1 rhodococcus
6	1151.5	64.9	348	2	Q9ZN85_9NOCA	Q9zn85 rhodococcus
7	1150.5	64.8	346	2	Q5YTY4_NOCFA	Q5yty4 nocardia fa
8	1100.5	62.0	348	2	Q47L68_THEFY	Q47l68 thermobifid
9	933.5	52.6	360	2	Q47PU4_THEFY	Q47pu4 thermobifid
10	881	49.6	343	2	Q46N63_RALEJ	Q46n63 ralstonia e
11	856.5	48.3	354	2	Q3H4C5_9ACTO	Q3h4c5 nocardioide
12	742.5	41.8	347	2	Q5YR32_NOCFA	Q5yr32 nocardia fa
13	704	39.7	359	2	Q5YXH9_NOCFA	Q5yxh9 nocardia fa
14	606	34.1	341	2	Q82NB0_STRAW	Q82nb0 streptomyce
15	579	32.6	347	2	Q3X235_9ACTN	Q3x235 rubrobacter
16	566	31.9	341	2	Q4J706_SULAC	Q4j706 sulfolobus
17	555.5	31.3	353	2	Q3WYQ7_9ACTN	Q3wyq7 rubrobacter
18	553	31.2	341	2	Q8CK64_STRCO	Q8ck64 streptomyce
19	552	31.1	341	2	Q2JA11_9ACTO	Q2ja11 frankia

RESULT 1

Q8KLT9_9NOCA

ID Q8KLT9_9NOCA PRELIMINARY; PRT; 346 AA.

AC Q8KLT9;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE Secondary alcohol dehydrogenase (EC 1.1.1.1).

GN Name=sadh;

OS Rhodococcus ruber.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI_TaxID=1830;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=219;

RA Tamak C., Plattner H., Hummel W., Diekmann H., Meens J.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- COFACTOR: Zinc (By similarity).

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

DR EMBL; AJ491307; CAD36475.1; -; Genomic_DNA.

DR HSSP; Q59096; 1F8F.

DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR013154; ADH_N.

DR InterPro; IPR002085; ADH_Sf_Zn.

DR InterPro; IPR002328; ADH_Zn.

DR InterPro; IPR013149; ADH_Zn_bd.

DR InterPro; IPR002110; ANK.

DR PANTHER; PTHR11695; Adh_zn_family; 1.

DR PRINTS; PR01415; ANKYRIN.

DR PROSITE; PS00059; ADH_ZINC; 1.

KW Metal-binding; NAD; Oxidoreductase; Zinc.

SQ SEQUENCE 346 AA; 35449 MW; F885D8B0F7E6C1CC CRC64;

Query Match 96.5%; Score 1713; DB 2; Length 346;
 Best Local Similarity 95.7%; Pred. No. 8.1e-102;
 Matches 330; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

```

Qy      1 MKAVQYTEIGSEPVVVDIPTPTPGPEILLKVTAAGLCHSDIFVMDMPAAQYAYGLPLTL 60
      |||:|||||||||||||:|||||
Db      1 MKALQYTEIGSEPVVVDVPTPAPGPGEILLKVTAAGLCHSDIFVMDMPAEQYIYGLPLTL 60

Qy     61 GHEGVGTVAELGEGVTGFGVGDAVAVYGPWGC GACHACARGRENYCTRAADLGITPPGLG 120
      |||:|||||||||||||:|||||
Db     61 GHEGVGTVAELGAGVTGFETGDAVAVYGPWGC GACHACARGRENYCTRAAELGITPPGLG 120

Qy    121 SPGSMAEYMIVDSARHLVPIGDLDPVAAAPLTDAGLTPYHAISRVLPLLGP GSTAVVIGV 180
      |||:|||||||||||||:|||||
Db    121 SPGSMAEYMIVDSARHLVPIGDLDPVAAVPLTDAGLTPYHAISRVLPLLGP GSTAVVIGV 180

Qy    181 GGLGHVGIQILRAVSAARVIAVDLDDRLALAREVGADAAVKSGAGAADAIRELTGGQGA 240
      |||:|||||||||||||:|||||
Db    181 GGLGHVGIQILRAVSAARVIAVDLDDRLALAREVGADAAVKSGAGAADAIRELTGGEGA 240

Qy    241 TAVFDFVGAQSTIDTAQQVVAVDGHISVVG IHAGAHAKVGFFMIPFGASVVTPYWGTRSE 300

```


Db	241	:	TAVFDFVGAQSTIDTAQQVVAIDGHISVVGIHAGAHAKVGFFMIPFGASVVTPYWGTRSE	300
Qy	301		LMEVVALARAGRLDIHTETFTLDEGPAAYRRLREGSIRGRGVVVP	345
Db	301	:	LMDVVDLARAGRLDIHTETFTLDEGPTAYRRLREGSIRGRGVVVP	345

RESULT 4

Q65YQ4_9NOCA

ID Q65YQ4_9NOCA PRELIMINARY; PRT; 348 AA.

AC Q65YQ4;

DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.

DT 25-OCT-2004, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Phenylacetaldehyde reductase.

GN Name=par;

OS Rhodococcus sp. ST-10.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI_TaxID=85582;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ST-10;

RX PubMed=16085867; DOI=10.1128/AEM.71.8.4713-4720.2005;

RA Makino Y., Inoue K., Dairi T., Itoh N.;

RT "Engineering of Phenylacetaldehyde Reductase for Efficient Substrate

RT Conversion in Concentrated 2-Propanol.";

RL Appl. Environ. Microbiol. 71:4713-4720(2005).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ST-10;

RX MEDLINE=20000646; PubMed=10531651; DOI=10.1007/s002530051536;

RA Wang J., Sakakibara M., Liu J., Dairi T., Itoh N.;

RT "Cloning, sequence analysis, and expression in Escherichia coli of the

RT gene encoding phenylacetaldehyde reductases from styrene-assimilating

RT Corynebacterium sp. ST-10.";

RL Appl. Microbiol. Biotechnol. 52:386-392(1999).

CC -!- COFACTOR: Zinc (By similarity).

CC

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC

DR EMBL; AB190261; BAD51480.1; -; Genomic_DNA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR013154; ADH_N.

DR InterPro; IPR002085; ADH_Sf_Zn.

DR InterPro; IPR002328; ADH_Zn.

DR InterPro; IPR013149; ADH_Zn_bd.

DR PANTHER; PTHR11695; Adh_zn_family; 1.

DR PROSITE; PS00059; ADH_ZINC; 1.

KW Metal-binding; NAD; Oxidoreductase; Zinc.

SQ SEQUENCE 348 AA; 36222 MW; 57568097CF806BEB CRC64;

Query Match 64.9%; Score 1152.5; DB 2; Length 348;

Best Local Similarity 63.6%; Pred. No. 6.9e-66;

Matches 220; Conservative 40; Mismatches 85; Indels 1; Gaps 1;

QY 1 MKAVQYTEIGSEPVVVDIPTPTPGPGGEILLKVTAAGLCHSDIFVMDMPAAQYAYGLPLTL 60

|||:|||| ||:|| : || | ||||:||||:||||:|||| | :| || |||||

Db 1 MKAIQYTRIGAEPTELTEIPKPEPGPGGEVLLEVTAAGVCHSDDFIMSLPEEQYTYGLPLTL 60

QY 61 GHEGVGTVAELGEGVTGFGVGDAVAVYGPWGCGACHACARGRENYCTRAADLGITPPGLG 120

|||| | || :|||| | :| | ||||| | | :|| ||||:|| :||| |||||

Db 61 GHEGAGKVAAVGEGVEGLDIGTNVVVYGPWGCGNCWHCSQGLENYCSRAQELGINPPGLG 120

QY 121 SPGSMAEYMIVDSARHLVPIGDLDPVAAAPLTDAGLTPYHAISRVLP LLGPGSTAVVIGV 180

Db	121	APGALAEFMIVDSPRHLVPIGDLDPVKTVPLTDAGLTPYHAIKRSLPKLRGGSYAVVIGT	180
Qy	181	GGLGHVGIQILRAVSAARVIAVDLDDRLALAREVGADAAVKSAGAGAADAIRELTGGQGA	240
Db	181	GGLGHVAIQLLRHLASAATVIALDVSADKLELATKVGAEHVVLSDKDAAENVRKITGSQGA	240
Qy	241	TAVFDFVGAQSTIDTAQQVVAVDGHISVVGIIHAG-AHAKVGFFMIPFGASVVTPYWGTRS	299
Db	241	ALVLDFVGYQPTIDTAMAVAGVGS DVTIVGIGDGAHAKVGFFQSPYEASVTVPYWGARN	300
Qy	300	ELMEVVALARAGRLDIHTETFTLDEGPAAYRRLREGSIRGRGVVVP	345
Db	301	ELIELIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTLSGRAVVVP	346

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	9	100.0	10	7	ADD44401	Add44401 Rhodococc
2	9	100.0	10	9	ADY85159	Ady85159 Rhodococc
3	8	88.9	248	8	ADX93553	Adx93553 Plant ful
4	8	88.9	267	8	ADX87812	Adx87812 Plant ful
5	8	88.9	268	8	ADX88645	Adx88645 Plant ful
6	8	88.9	345	9	ADY85204	Ady85204 Rhodococc
7	8	88.9	799	7	ABM88577	Abm88577 Rice abio
8	7	77.8	106	3	AAG26730	Aag26730 Zea mays
9	7	77.8	123	3	AAY81132	Aay81132 Neisseria
10	7	77.8	123	3	AAY81131	Aay81131 Neisseria
11	7	77.8	123	6	ABP80703	Abp80703 N. gonorr
12	7	77.8	123	6	ABU37479	Abu37479 Protein e
13	7	77.8	123	6	ABU37710	Abu37710 Protein e
14	7	77.8	123	8	ADP08183	Adp08183 Neisseria
15	7	77.8	137	3	AAG26729	Aag26729 Zea mays
16	7	77.8	137	8	ADQ09964	Adq09964 Borrelia
17	7	77.8	171	7	ABO71893	Abo71893 Pseudomon

Database : Issued_Patents_AA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	7	77.8	171	2	US-09-252-991A-20639	Sequence 20639, A
2	7	77.8	233	2	US-09-252-991A-26632	Sequence 26632, A
3	7	77.8	298	2	US-09-252-991A-22985	Sequence 22985, A
4	7	77.8	414	2	US-09-252-991A-17165	Sequence 17165, A
5	7	77.8	485	2	US-09-252-991A-24868	Sequence 24868, A
6	7	77.8	614	2	US-09-252-991A-20210	Sequence 20210, A
7	7	77.8	717	2	US-09-252-991A-22029	Sequence 22029, A
8	7	77.8	743	2	US-09-252-991A-28327	Sequence 28327, A
9	6	66.7	118	2	US-08-301-162-10	Sequence 10, Appl
10	6	66.7	118	2	US-09-461-240-10	Sequence 10, Appl
11	6	66.7	118	2	US-09-968-927-10	Sequence 10, Appl
12	6	66.7	133	2	US-09-252-991A-30896	Sequence 30896, A
13	6	66.7	139	2	US-09-270-767-35479	Sequence 35479, A
14	6	66.7	139	2	US-09-270-767-50696	Sequence 50696, A
15	6	66.7	150	2	US-09-252-991A-29818	Sequence 29818, A
16	6	66.7	169	2	US-09-252-991A-26193	Sequence 26193, A

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	7	77.8	123	2	H81235	50S ribosomal prot
2	7	77.8	255	2	JC7264	CCAAT-enhancer bin
3	7	77.8	263	2	B75361	WD-repeat family p
4	6	66.7	109	1	R6BY11	acidic ribosomal p
5	6	66.7	112	2	B43601	LSR2 T-cell antige
6	6	66.7	137	2	AD3645	flagella basal bod
7	6	66.7	161	2	E70867	hypothetical prote
8	6	66.7	183	2	T51910	hypothetical prote
9	6	66.7	184	2	C95930	conserved hypothet

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	8	88.9	346	2	Q8KLT9_9NOCA	Q8klt9 rhodococcus
2	8	88.9	557	2	Q2T4A0_BURTH	Q2t4a0 burkholderi
3	8	88.9	581	2	Q5KGT5_CRYNE	Q5kgt5 cryptococcu
4	8	88.9	613	2	Q55SE1_CRYNE	Q55se1 cryptococcu
5	7	77.8	73	2	Q7R475_GIALA	Q7r475 giardia lam
6	7	77.8	98	2	Q7Y1Q2_MAIZE	Q7ylq2 zea mays (m
7	7	77.8	99	2	Q4P9Q4_USTMA	Q4p9q4 ustilago ma
8	7	77.8	122	1	RL7_NEIMA	P0a0x0 neisseria m
9	7	77.8	122	1	RL7_NEIMB	P0a0x1